

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/574,827  
Source: IFWP  
Date Processed by STIC: 5/4/06

# ***ENTERED***



IFWP

## RAW SEQUENCE LISTING

DATE: 05/04/2006

PATENT APPLICATION: US/10/574,827

TIME: 13:36:02

Input Set : A:\14875-158US1sq.txt

Output Set: N:\CRF4\05042006\J574827.raw

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3 <110> APPLICANT: Hayasaka, Akira
4     Igawa, Tomoyuki
5     Sekimori, Yasuo
8 <120> TITLE OF INVENTION: Method of stabilizing protein solutions
10 <130> FILE REFERENCE: 14875-158US1
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/574,827
C--> 12 <141> CURRENT FILING DATE: 2006-04-06
12 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/014919
13 <151> PRIOR FILING DATE: 2004-10-08
15 <150> PRIOR APPLICATION NUMBER: JP 2003-351410
16 <151> PRIOR FILING DATE: 2003-10-09
18 <160> NUMBER OF SEQ ID NOS: 18
20 <170> SOFTWARE: PatentIn version 3.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1779
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (1)..(1779)
30 <223> OTHER INFORMATION:
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34 Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
35 1          5          10          15
37 gtc cag tgt gag gtg cag ctg ttg gat tct ggg gga ggc ttg gta cag      96
38 Val Gln Cys Glu Val Gln Leu Leu Asp Ser Gly Gly Gly Leu Val Gln
39          20          25          30
41 cct ggg ggg tgc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt      144
42 Pro Gly Gly Cys Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
43          35          40          45
45 agc agc tgt gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg      192
46 Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
47          50          55          60
49 gag tgg gtc tca gct att agt ggt agt ggt ggt agc aca tac tac gca      240
50 Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala
51 65          70          75          80
53 gac tcc gtg aag ggc cgg ttc acc atc tcc aga gac aaa tcc aag aac      288
54 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Lys Asn
55          85          90          95
57 acg ttg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gta      336
58 Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
59          100          105          110

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61 tat tac tgt gcg aaa ggt ggc aac gat att ttg act ggt tat tat gct      384
62 Tyr Tyr Cys Ala Lys Gly Gly Asn Asp Ile Leu Thr Gly Tyr Tyr Ala
63      115      120      125
65 tgg ggc cag gga acc ctg gtc acc gtc tcc tca ggg agt gca tcc gcc      432
66 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Ala Ser Ala
67      130      135      140
69 cca acc ctt ttc ccc ctc gtc tcc tgt gag aat tcc ccg tcc gat agc      480
70 Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr
71 145      150      155      160
73 agc agc gtg gcc gtt ggc tgc ctc gca cag gac ttc ctt ccc gac tcc      528
74 Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu Pro Asp Ser
75      165      170      175
77 atc act ttc tcc tgg aaa tac aag aac aac tct gac atc agc agc acc      576
78 Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile Ser Ser Thr
79      180      185      190
81 cgg ggc ttc cca tca gtc ctg aga ggg ggc aag tac gca gcc acc tca      624
82 Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala Ala Thr Ser
83      195      200      205
85 cag gtg ctg ctg cct tcc aag gac gtc atg cag ggc aca gac gag cac      672
86 Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr Asp Glu His
87      210      215      220
89 gtg gtg tgc aaa gtc cag cac ccc aac ggc aac aaa gaa aag aac gtg      720
90 Val Val Cys Lys Val Gln His Pro Asn Gly Asn Lys Glu Lys Asn Val
91 225      230      235      240
93 cct ctt cca gtg att gct gag ctg cct ccc aaa gtg agc gtc ttc gtc      768
94 Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val
95      245      250      255
97 cca ccc cgc gac ggc ttc ttc ggc aac ccc cgc aag tcc aag ctc atc      816
98 Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile
99      260      265      270
101 tgc cag gcc acg ggt ttc agt ccc cgg cag att cag gtg tcc tgg ctg      864
102 Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu
103      275      280      285
105 cgc gag ggg aag cag gtg ggg tct ggc gtc acc acg gac cag gtg cag      912
106 Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln
107      290      295      300
109 gct gag gcc aaa gag tct ggg ccc acg acc tac aag gtg acc agc aca      960
110 Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr
111 305      310      315      320
113 ctg acc atc aaa gag agc gac tgg ctc ggc cag agc atg ttc acc tgc      1008
114 Leu Thr Ile Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys
115      325      330      335
117 cgc gtg gat cac agg ggc ctg acc ttc cag cag aat gcg tcc tcc atg      1056
118 Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met
119      340      345      350
121 tgt gtc ccc gat caa gac aca gcc atc cgg gtc ttc gcc atc ccc cca      1104
122 Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro
123      355      360      365
125 tcc ttt gcc agc atc ttc ctc acc aag tcc acc aag ttg acc tgc ctg      1152

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126 Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu
127      370      375      380
129 gtc aca gac ctg acc acc tat gac agc gtg acc atc tcc tgg acc cgc      1200
130 Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg
131 385      390      395      400
133 cag aat ggc gaa gct gtg aaa acc cac acc aac atc tcc gag agc cac      1248
134 Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His
135      405      410      415
137 ccc aat gcc act ttc agc gcc gtg ggt gag gcc agc atc tgc gag gat      1296
138 Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp
139      420      425      430
141 gac tgg aat tcc ggg gag agg ttc acg tgc acc gtg acc cac aca gac      1344
142 Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp
143      435      440      445
145 ctg ccc tgc cca ctg aag cag acc atc tcc cgg ccc aag ggg gtg gcc      1392
146 Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Val Ala
147      450      455      460
149 ctg cac agg ccc gat gtc tac ttg ctg cca cca gcc cgg gag cag ctg      1440
150 Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu
151 465      470      475      480
153 aac ctg cgg gag tgc gcc acc atc acg tgc ctg gtg acg ggc ttc tct      1488
154 Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly Phe Ser
155      485      490      495
157 ccc gcg gac gtc ttc gtg cag tgg atg cag agg ggg cag ccc ttg tcc      1536
158 Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro Leu Ser
159      500      505      510
161 ccg gag aag tat gtg acc agc gcc cca atg cct gag ccc cag gcc cca      1584
162 Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln Ala Pro
163      515      520      525
165 ggc cgg tac ttc gcc cac agc atc ctg acc gtg tcc gaa gag gaa tgg      1632
166 Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu Glu Trp
167      530      535      540
169 aac acg ggg gag acc tac acc tgc gtg gtg gcc cat gag gcc ctg ccc      1680
170 Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro
171 545      550      555      560
173 aac agg gtc acc gag agg acc gtg gac aag tcc acc ggt aaa ccc acc      1728
174 Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly Lys Pro Thr
175      565      570      575
177 ctg tac aac gtg tcc ctg gtc atg tcc gac aca gct ggc acc tgc tac      1776
178 Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly Thr Cys Tyr
179      580      585      590
181 tga      1779
184 <210> SEQ ID NO: 2
185 <211> LENGTH: 592
186 <212> TYPE: PRT
187 <213> ORGANISM: Homo sapiens
189 <400> SEQUENCE: 2
190 Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
191 1      5      10      15

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192 Val Gln Cys Glu Val Gln Leu Leu Asp Ser Gly Gly Gly Leu Val Gln
193      20      25      30
194 Pro Gly Gly Cys Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
195      35      40      45
196 Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
197      50      55      60
198 Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala
199      65      70      75      80
200 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Lys Asn
201      85      90      95
202 Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
203      100     105     110
204 Tyr Tyr Cys Ala Lys Gly Gly Asn Asp Ile Leu Thr Gly Tyr Tyr Ala
205      115     120     125
206 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Ala Ser Ala
207      130     135     140
208 Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr
209      145     150     155     160
210 Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu Pro Asp Ser
211      165     170     175
212 Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile Ser Ser Thr
213      180     185     190
214 Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala Ala Thr Ser
215      195     200     205
216 Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr Asp Glu His
217      210     215     220
218 Val Val Cys Lys Val Gln His Pro Asn Gly Asn Lys Glu Lys Asn Val
219      225     230     235     240
220 Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val
221      245     250     255
222 Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile
223      260     265     270
224 Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu
225      275     280     285
226 Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln
227      290     295     300
228 Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr
229      305     310     315     320
230 Leu Thr Ile Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys
231      325     330     335
232 Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met
233      340     345     350
234 Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro
235      355     360     365
236 Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu
237      370     375     380
238 Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg
239      385     390     395     400
240 Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His

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TIME: 13:36:02

Input Set : A:\14875-158US1sq.txt

Output Set: N:\CRF4\05042006\J574827.raw

```

241          405          410          415
242 Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp
243          420          425          430
244 Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp
245          435          440          445
246 Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Val Ala
247          450          455          460
248 Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu
249 465          470          475          480
250 Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly Phe Ser
251          485          490          495
252 Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro Leu Ser
253          500          505          510
254 Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln Ala Pro
255          515          520          525
256 Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu Glu Trp
257          530          535          540
258 Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro
259 545          550          555          560
260 Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly Lys Pro Thr
261          565          570          575
262 Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly Thr Cys Tyr
263          580          585          590

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266 &lt;210&gt; SEQ ID NO: 3

267 &lt;211&gt; LENGTH: 723

268 &lt;212&gt; TYPE: DNA

269 &lt;213&gt; ORGANISM: Homo sapiens

271 &lt;220&gt; FEATURE:

272 &lt;221&gt; NAME/KEY: CDS

273 &lt;222&gt; LOCATION: (1)..(723)

274 &lt;223&gt; OTHER INFORMATION:

W--&gt; 276 &lt;400&gt; 3

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277 atg gtg ttg cag acc cag gtc ttc att tct ctg ttg ctc tgg atc tct      48
278 Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
279 1          5          10          15
281 ggt gcc tac ggg gac atc gtg atg acc cag tct cca gac tcc ctg gct      96
282 Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
283          20          25          30
285 gtg tct ctg ggc gag agg gcc acc atc aac tgc aag tcc agc cag agt     144
286 Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser
287          35          40          45
289 gtt tta tac agc tcc aac aat aag aac tac tta gct tgg tac cag cag     192
290 Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
291          50          55          60
293 aaa cca gga cag cct cct aag ctg ctc att tac tgg gca tct acc cgg     240
294 Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
295 65          70          75          80
297 gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg tct ggg aca gat     288
298 Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp

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RAW SEQUENCE LISTING ERROR SUMMARY

DATE: 05/04/2006

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TIME: 13:36:03

Input Set : A:\14875-158US1sq.txt

Output Set: N:\CRF4\05042006\J574827.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:7,8,9,10,11,12,13,14,15,16,17,18

## VERIFICATION SUMMARY

DATE: 05/04/2006

PATENT APPLICATION: US/10/574,827

TIME: 13:36:03

Input Set : A:\14875-158US1sq.txt

Output Set: N:\CRF4\05042006\J574827.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:32 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:30  
L:276 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:274  
L:388 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:386